SEQUENCE LISTING

(1) GENERAL INFORMATION:

    (i) APPLICANT: Huse, William D.
                Glaser, Scott M.

    (ii) TITLE OF INVENTION: Anti-Alpha V Beta 3 Recombinant Human
          Antibodies, Nucleic Acids Encoding Same and Methods of Use

    (iii) NUMBER OF SEQUENCES: 100

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    (v) COMPUTER READABLE FORM:
        (A) MEDIUM TYPE: Floppy disk
        (B) COMPUTER: IBM PC compatible
        (C) OPERATING SYSTEM: PC-DOS/MS-DOS
        (D) SOFTWARE: PatentIn Release #1.0, Version #1.25

    (vi) CURRENT APPLICATION DATA:
        (A) APPLICATION NUMBER: US 09/016,061
        (B) FILING DATE: 30-JAN-1998
        (C) CLASSIFICATION:

    (vii) PRIOR APPLICATION DATA:
        (A) APPLICATION NUMBER: US 08/791,391
        (B) FILING DATE: 30-JAN-1997

    (viii) ATTORNEY/AGENT INFORMATION:
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        (C) REFERENCE/DOCKET NUMBER: P-IX 2965

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(2) INFORMATION FOR SEQ ID NO:1:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 351 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..351

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:1:

```
CAG GTG CAG CTG GTG GAG TCT GGG GGA GGC GTT GTG CAG CCT GGA AGG        48
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1               5                  10                  15
```

```
TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC ACC TTC AGT AGC TAT          96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
        20                  25                  30

GAC ATG TCT TGG GTT CGC CAG GCT CCG GGC AAG GGT CTG GAG TGG GTC         144
Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG         192
Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
        50                  55                  60

CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT AGT AAG AAC ACC CTA TAC         240
Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65·                 70                  75                  80

CTG CAA ATG AAC TCT CTG AGA GCC GAG GAC ACA GCC GTG TAT TAC TGT         288
Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT ACA         336
Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
                100                 105                 110

GTG ACT GTT TCT AGT                                                     351
Val Thr Val Ser Ser
        115
```

(2) INFORMATION FOR SEQ ID NO:2:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 117 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:2:

```
Gln Val Gln Leu Val Glu Ser Gly Gly Gly Val Val Gln Pro Gly Arg
 1·              5               10                  15

Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Thr Phe Ser Ser Tyr
        20                  25                  30

Asp Met Ser Trp Val Arg Gln Ala Pro Gly Lys Gly Leu Glu Trp Val
        35                  40                  45

Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
        50                  55                  60

Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ser Lys Asn Thr Leu Tyr
65                  70                  75                  80

Leu Gln Met Asn Ser Leu Arg Ala Glu Asp Thr Ala Val Tyr Tyr Cys
                85                  90                  95

Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Thr
                100                 105                 110

Val Thr Val Ser Ser
        115
```

(2) INFORMATION FOR SEQ ID NO:3:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 321 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..321

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:3:

```
GAG ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT CTC AGC CCA GGA      48
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1               5                  10                  15

GAA AGG GCG ACT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC      96
Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
                20                  25                  30

CTA CAC TGG TAT CAA CAA AGG CCT GGT CAA GCC CCA AGG CTT CTC ATC     144
Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
                35                  40                  45

AAG TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC GCC AGG TTC AGT GGC     192
Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
                50                  55                  60

AGT GGA TCA GGG ACA GAT TTC ACC CTC ACT ATC TCC AGT CTG GAG CCT     240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65                  70                  75                  80

GAA GAT TTT GCA GTC TAT TAC TGT CAA CAG AGT GGC AGC TGG CCT CAC     288
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
                    85                  90                  95

ACG TTC GGA GGG GGG ACC AAG GTG GAA ATT AAG                         321
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
                100                 105
```


(2) INFORMATION FOR SEQ ID NO:4:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 107 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:4:

```
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
 1               5                  10                  15

Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
                20                  25                  30

Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
                35                  40                  45

Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
                50                  55                  60
```

```
Ser. Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65            70                75                    80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
            85                90                    95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100              .105
```

(2) INFORMATION FOR SEQ ID NO:5:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 351 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: both
         (D) TOPOLOGY: linear

      (ix) FEATURE:
         (A) NAME/KEY: CDS
         (B) LOCATION: 1..351

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:5:

```
GAA GTG CAG CTG GTG GAG TCT GGG GGA GGC TTA GTG AAG CCT GGA AGG      48
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
1.              5                 10                  15

TCC CTG AGA CTC TCC TGT GCA GCC TCT GGA TTC GCT TTC AGT AGC TAT      96
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
            20              .           25                  30

GAC ATG TCT TGG GTT CGC CAG ATT CCG GAG AAG AGG CTG GAG TGG GTC     144
Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
            35                  40                  45

GCA AAA GTT AGT AGT GGT GGT GGT AGC ACC TAC TAT TTA GAC ACT GTG     192
Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
    50                  55                  60

CAG GGC CGA TTC ACC ATC TCC AGA GAC AAT GCC AAG AAC ACC CTA TAC     240
Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80

CTG CAA ATG AGC AGT CTG AAC TCT GAG GAC ACA GCC ATG TAT TAC TGT     288
Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95

GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC TGG GGC CAA GGG ACT CTG     336
Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
            100                 105                 110

GTC ACT GTC TCT GCA                                                  351
Val. Thr Val Ser Ala
        115
```

(2) INFORMATION FOR SEQ ID NO:6:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 117 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:6:

```
Glu Val Gln Leu Val Glu Ser Gly Gly Gly Leu Val Lys Pro Gly Arg
 1               5                  10                  15
```

```
Ser Leu Arg Leu Ser Cys Ala Ala Ser Gly Phe Ala Phe Ser Ser Tyr
            20                  25                  30
```

```
Asp Met Ser Trp Val Arg Gln Ile Pro Glu Lys Arg Leu Glu Trp Val
        35                  40                  45
```

```
Ala Lys Val Ser Ser Gly Gly Gly Ser Thr Tyr Tyr Leu Asp Thr Val
    50                  55                  60
```

```
Gln Gly Arg Phe Thr Ile Ser Arg Asp Asn Ala Lys Asn Thr Leu Tyr
65                  70                  75                  80
```

```
Leu Gln Met Ser Ser Leu Asn Ser Glu Asp Thr Ala Met Tyr Tyr Cys
                85                  90                  95
```

```
Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr Trp Gly Gln Gly Thr Leu
                100                 105                 110
```

```
Val Thr Val Ser Ala
            115
```

(2) INFORMATION FOR SEQ ID NO:7:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 321 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..321

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:7:

```
GAT ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT GTG ACA CCA GGA     48
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
 1               5                  10                  15
```

```
GAT AGC GTC AGT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC     96
Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
            20                  25                  30
```

```
CTA CAC TGG TAT CAA CAA AAA TCA CAT GAG TCT CCA AGG CTT CTC ATC    144
Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
            35                  40                  45
```

```
AAG TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC TCC AGG TTC AGT GGC    192
Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60
```

```
AGT GGA TCA GGG ACA GAT TTC GCT CTC AGT ATC AAC AGT GTG GAG ACT    240
Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr
65                  70                  75                  80
```

```
GAA GAT TTT GGA ATG TAT TTC TGT CAA CAG AGT GGC AGC TGG CCT CAC    288
Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His
                85                  90                  95
```

```
ACG TTC GGA GGG GGG ACC AAG CTG GAA ATT AAG                        321
```

```
Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:8:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 107 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:8:

```
Asp Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Val Thr Pro Gly
 1               5                  10                  15

Asp Ser Val Ser Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
            20                  25                  30

Leu His Trp Tyr Gln Gln Lys Ser His Glu Ser Pro Arg Leu Leu Ile
            35                  40                  45

Lys Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ser Arg Phe Ser Gly
    50                  55                  60

Ser Gly Ser Gly Thr Asp Phe Ala Leu Ser Ile Asn Ser Val Glu Thr
 65                  70                  75                  80

Glu Asp Phe Gly Met Tyr Phe Cys Gln Gln Ser Gly Ser Trp Pro His
            85                  90                  95

Thr Phe Gly Gly Gly Thr Lys Leu Glu Ile Lys
            100                 105
```

(2) INFORMATION FOR SEQ ID NO:9:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 84 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: both
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:9:

```
CAGGTGCAGC TGGTGGAGTC TGGGGGAGGC GTTGTGCAGC CTGGAAGGTC CCTGAGACTC    60

TCCTGTGCAG CCTCTGGATT CACC                                          84
```

(2) INFORMATION FOR SEQ ID NO:10:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 84 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: both
          (D) TOPOLOGY: linear

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:10:

```
AACTTTTGCG ACCCACTCCA GACCCTTGCC CGGAGCCTGG CGAACCCAAG ACATGTCATA    60

GCTACTGAAG GTGAATCCAG AGGC                                          84
```

(2) INFORMATION FOR SEQ ID NO:11:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 87 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:11:

TGGGTCGCAA AAGTTAGTAG TGGTGGTGGT AGCACCTACT ATTTAGACAC TGTGCAGGGC   60

CGATTCACCA TCTCCAGAGA CAATAGT   87

(2) INFORMATION FOR SEQ ID NO:12:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 81 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:12:

TGCACAGTAA TACACGGCTG TGTCCTCGGC TCTCAGAGAG TTCATTTGCA GGTATAGGGT   60

GTTCTTACTA TTGTCTCTGG A   81

(2) INFORMATION FOR SEQ ID NO:13:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 75 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:13:

GTGTATTACT GTGCAAGACA TAACTACGGC AGTTTTGCTT ACTGGGGCCA AGGGACTACA   60

GTGACTGTTT CTAGT   75

(2) INFORMATION FOR SEQ ID NO:14:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 87 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:14:

GAGATTGTGC TAACTCAGTC TCCAGCCACC CTGTCTCTCA GCCCAGGAGA AAGGGCGACT   60

CTTTCCTGCC AGGCCAGCCA AAGTATT   87

(2) INFORMATION FOR SEQ ID NO:15:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 72 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:15:

GATGAGAAGC CTTGGGGCTT GACCAGGCCT TTGTTGATAC CAGTGTAGGT GGTTGCTAAT   60

ACTTTGGCTG GC   72

(2) INFORMATION FOR SEQ ID NO:16:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 84 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:16:

CCAAGGCTTC TCATCWASTA TCGTTCCCAG TCCATCTCTG GGATCCCCGC CAGGTTCAGT   60

GGCAGTGGAT CAGGGACAGA TTTC   84

(2) INFORMATION FOR SEQ ID NO:17:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 81 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:17:

GCTGCCACTC TGTTGACAGW AATAGACTGC AAAATCTTCA GGCTCCAGAC TGGAGATAGT   60

GAGGGTGAAA TCTGTCCCTG A   81

(2) INFORMATION FOR SEQ ID NO:18:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 57 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:18:

CAACAGAGTG GCAGCTGGCC TCACACGTTC GGAGGGGGGA CCAAGGTGGA AATTAAG   57

(2) INFORMATION FOR SEQ ID NO:19:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:19:

GCCCAACCAG CCATGGCCGA TATTGTGCTA ACTCAG   36

(2) INFORMATION FOR SEQ ID NO:20:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:20:

ACAGTTGGTG CAGCATCAGC   20

(2) INFORMATION FOR SEQ ID NO:21:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 36 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:21:

ACCCCTGTGG CAAAAGCCGA AGTGCAGCTG GTGGAG   36

(2) INFORMATION FOR SEQ ID NO:22:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 20 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:22:

GATGGGGGTG TCGTTTTGGC   20

(2) INFORMATION FOR SEQ ID NO:23:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 87 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:23:

GAGATTGTGC TAACTCAGTC TCCAGCCACC CTGTCTCTCA GCCCAGGAGA AAGGGCGACT   60

CTTTCCTGCC AGGCCAGCCA AAGTATT   87

(2) INFORMATION FOR SEQ ID NO:24:

```
      (i)  SEQUENCE CHARACTERISTICS:
           (A)  LENGTH: 75 base pairs
           (B)  TYPE: nucleic acid
           (C)  STRANDEDNESS: both
           (D)  TOPOLOGY: linear


      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:24:

TTAGATGAGA AGCCTTGGGG CTTGACCAGG CCTTTGTTGA TACCAGTGTA GGTGGTTGCT          60

AATACTTTGG CTGGC                                                           75

(2)  INFORMATION FOR SEQ ID NO:25:

      (i)  SEQUENCE CHARACTERISTICS:
           (A)  LENGTH: 84 base pairs
           (B)  TYPE: nucleic acid
           (C)  STRANDEDNESS: both
           (D)  TOPOLOGY: linear


      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:25:

CCAAGGCTTC TCATCTAATA TCGTTCCCAG TCCATCTCTG GGATCCCCGC CAGGTTCAGT          60

GGCAGTGGAT CAGGGACAGA TTTC                                                 84

(2)  INFORMATION FOR SEQ ID NO:26:

      (i)  SEQUENCE CHARACTERISTICS:
           (A)  LENGTH: 81 base pairs
           (B)  TYPE: nucleic acid
           (C)  STRANDEDNESS: both
           (D)  TOPOLOGY: linear


      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:26:

GCTGCCACTC TGTTGACAGT AATAGACTGC AAAATCTTCA GGCTCCAGAC TGGAGATAGT          60

GAGGGTGAAA TCTGTCCCTG A                                                    81

(2)  INFORMATION FOR SEQ ID NO:27:

      (i)  SEQUENCE CHARACTERISTICS:
           (A)  LENGTH: 57 base pairs
           (B)  TYPE: nucleic acid
           (C)  STRANDEDNESS: both
           (D)  TOPOLOGY: linear


      (xi)  SEQUENCE DESCRIPTION: SEQ ID NO:27:

CAACAGAGTG GCAGCTGGCC TCACACGTTC GGAGGGGGGA CCAAGGTGGA AATTAAG            57

(2)  INFORMATION FOR SEQ ID NO:28:

      (i)  SEQUENCE CHARACTERISTICS:
           (A)  LENGTH: 10 amino acids
           (B)  TYPE: amino acid
           (D)  TOPOLOGY: linear
```

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:28:

```
Tyr Pro Tyr Asp Val Pro Asp Tyr Ala Ser
1               5               10
```

(2) INFORMATION FOR SEQ ID NO:29:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 22 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:29:

GCTACTGAAG GCGAATCCAG AG   22

(2) INFORMATION FOR SEQ ID NO:30:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 23 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: misc_feature
        (B) LOCATION: 11..13
        (D) OTHER INFORMATION: /note= ""NNN" represents a codon
                specifying any amino acid other than Lys."

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:30:

GGGAACGATA NNNGATGAGA AGC   23

(2) INFORMATION FOR SEQ ID NO:31:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 321 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: single
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..321

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:31:

```
GAG ATT GTG CTA ACT CAG TCT CCA GCC ACC CTG TCT CTC AGC CCA GGA      48
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5               10                  15

GAA AGG GCG ACT CTT TCC TGC CAG GCC AGC CAA AGT ATT AGC AAC CAC      96
Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
            20              25              30

CTA CAC TGG TAT CAA CAA AGG CCT GGT CAA GCC CCA AGG CTT CTC ATC      144
Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35              40              45
```

```
MKK TAT CGT TCC CAG TCC ATC TCT GGG ATC CCC GCC AGG TTC AGT GGC    192
Xaa Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
    50              55              60

AGT GGA TCA GGG ACA GAT TTC ACC CTC ACT ATC TCC AGT CTG GAG CCT    240
Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65·             70              75                          80

GAA GAT TTT GCA GTC TAT TAC TGT CAA CAG AGT GGC AGC TGG CCT CAC    288
Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
                85              90              95

ACG TTC GGA GGG GGG ACC AAG GTG GAA ATT AAG                        321
Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100             105
```

(2) INFORMATION FOR SEQ ID NO:32:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 107 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:32:

```
Glu Ile Val Leu Thr Gln Ser Pro Ala Thr Leu Ser Leu Ser Pro Gly
1               5               10              15

Glu Arg Ala Thr Leu Ser Cys Gln Ala Ser Gln Ser Ile Ser Asn His
        20              ·25             30

Leu His Trp Tyr Gln Gln Arg Pro Gly Gln Ala Pro Arg Leu Leu Ile
        35              40              45

Xaa Tyr Arg Ser Gln Ser Ile Ser Gly Ile Pro Ala Arg Phe Ser Gly
    50              55              60

Ser Gly Ser Gly Thr Asp Phe Thr Leu Thr Ile Ser Ser Leu Glu Pro
65              70              75                          80

Glu Asp Phe Ala Val Tyr Tyr Cys Gln Gln Ser Gly Ser Trp Pro His
                85              90              95

Thr Phe Gly Gly Gly Thr Lys Val Glu Ile Lys
            100             105
```

(2) INFORMATION FOR SEQ ID NO:33:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 30 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: both
          (D) TOPOLOGY: linear

      (ix) FEATURE:
          (A) NAME/KEY: CDS·
          (B) LOCATION: 1..30

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:33:

```
GGA TTC ACC TTC AGT AGC TAT GAC ATG TCT                            30
Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser
1               5               10
```

(2) INFORMATION FOR SEQ ID NO:34:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:34:

Gly Phe Thr Phe Ser Ser Tyr Asp Met Ser
1   5   10

(2) INFORMATION FOR SEQ ID NO:35:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..30

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:35:

TGG GTC GCA AAA GTT AGT AGT GGT GGT GGT   30
Trp Val Ala Lys Val Ser Ser Gly Gly Gly
1   5   10

(2) INFORMATION FOR SEQ ID NO:36:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:36:

Trp Val Ala Lys Val Ser Ser Gly Gly Gly
1   5   10

(2) INFORMATION FOR SEQ ID NO:37:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..30

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:37:

AGC ACC TAC TAT TTA GAC ACT GTG CAG GGC   30
Ser Thr Tyr Tyr Leu Asp Thr Val Gln Gly
1   5   10

(2) INFORMATION FOR SEQ ID NO:38:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 10 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:38:

Ser Thr Tyr Tyr Leu Asp Thr Val Gln Gly
1   5   10

(2) INFORMATION FOR SEQ ID NO:39:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 30 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: both
         (D) TOPOLOGY: linear

      (ix) FEATURE:
         (A) NAME/KEY: CDS
         (B) LOCATION: 1..30

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:39:

GCA AGA CAT AAC TAC GGC AGT TTT GCT TAC   30
Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr
1   5   10

(2) INFORMATION FOR SEQ ID NO:40:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 10 amino acids
         (B) TYPE: amino acid
         (D) TOPOLOGY: linear

      (ii) MOLECULE TYPE: protein

      (xi) SEQUENCE DESCRIPTION: SEQ ID NO:40:

Ala Arg His Asn Tyr Gly Ser Phe Ala Tyr
1   5   10

(2) INFORMATION FOR SEQ ID NO:41:

      (i) SEQUENCE CHARACTERISTICS:
         (A) LENGTH: 39 base pairs
         (B) TYPE: nucleic acid
         (C) STRANDEDNESS: both
         (D) TOPOLOGY: linear

      (ix) FEATURE:
         (A) NAME/KEY: CDS

(B) LOCATION: 1..39

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:41:

```
CAG GCC AGC CAA AGT ATT AGC AAC CAC CTA CAC TGG TAT                    39
Gln Ala Ser Gln Ser Ile Ser Asn His Leu His Trp Tyr
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:42:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 13 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:42:

```
Gln Ala Ser Gln Ser Ile Ser Asn His Leu His Trp Tyr
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:43:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 33 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..33

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:43:

```
CTT CTC ATC CGT TAT CGT TCC CAG TCC ATC TCT                    33
Leu Leu Ile Arg Tyr Arg Ser Gln Ser Ile Ser
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:44:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 11 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:44:

```
Leu Leu Ile Arg Tyr Arg Ser Gln Ser Ile Ser
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:45:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 27 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

```
    (ix) FEATURE:
         (A) NAME/KEY: CDS
         (B) LOCATION: 1..27


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:45:

CAA CAG AGT GGC AGC TGG CCT CAC ACG                              27
Gln Gln Ser Gly Ser Trp Pro His Thr
  1               5


(2) INFORMATION FOR SEQ ID NO:46:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 9 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:46:

Gln Gln Ser Gly Ser Trp Pro His Thr
  1               5

(2) INFORMATION FOR SEQ ID NO:47:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 30 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: both
            (D) TOPOLOGY: linear


       (ix) FEATURE:
            (A) NAME/KEY: CDS
            (B) LOCATION: 1..30


       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:47:

GGA ACT ACC TTC AGT AGC TAT GAC ATG TCT                          30
Gly Thr Thr Phe Ser Ser Tyr Asp Met Ser
  1               5                   10


(2) INFORMATION FOR SEQ ID NO:48:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 10 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:48:

Gly Thr Thr Phe Ser Ser Tyr Asp Met Ser
  1               5                   10

(2) INFORMATION FOR SEQ ID NO:49:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 30 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: both
```

```
            (D) TOPOLOGY: linear


    (ix) FEATURE:
            (A) NAME/KEY: CDS
            (B) LOCATION: 1..30


    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:49:

GGA TTC ACC TGG AGT AGC TAT GAC ATG TCT                              30
Gly Phe Thr Trp Ser Ser Tyr Asp Met Ser
 1               5                   10


(2) INFORMATION FOR SEQ ID NO:50:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 10 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:50:

Gly Phe Thr Trp Ser Ser Tyr Asp Met Ser
 1               5                   10

(2) INFORMATION FOR SEQ ID NO:51:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 30 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: both
            (D) TOPOLOGY: linear


    (ix) FEATURE:
            (A) NAME/KEY: CDS
            (B) LOCATION: 1..30


  . (xi) SEQUENCE DESCRIPTION: SEQ ID NO:51:

GGA TTC ACC TTC CTG AGC TAT GAC ATG TCT                              30
Gly Phe Thr Phe Leu Ser Tyr Asp Met Ser
 1               5                   10


(2) INFORMATION FOR SEQ ID NO:52:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 10 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

       (ii) MOLECULE TYPE: protein

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:52:

Gly Phe Thr Phe Leu Ser Tyr Asp Met Ser
 1               5                   10

(2) INFORMATION FOR SEQ ID NO:53:
```

```
(i)  SEQUENCE CHARACTERISTICS:
     (A)  LENGTH: 30 base pairs
     (B)  TYPE: nucleic acid
     (C)  STRANDEDNESS: both
     (D)  TOPOLOGY: linear


(ix) FEATURE:
     (A)  NAME/KEY: CDS
     (B)  LOCATION: 1..30


(xi) SEQUENCE DESCRIPTION: SEQ ID NO:53:

TGG GTC GCA AAA GTT AAA AGT GGT GGT GGT                                    30
Trp Val Ala Lys Val Lys Ser Gly Gly Gly
 1               5                   10


(2) INFORMATION FOR SEQ ID NO:54:

     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 10 amino acids
          (B)  TYPE: amino acid
          (D)  TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:54:

Trp Val Ala Lys Val Lys Ser Gly Gly Gly
 1               5                   10

(2) INFORMATION FOR SEQ ID NO:55:

     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 30 base pairs
          (B)  TYPE: nucleic acid
          (C)  STRANDEDNESS: both
          (D)  TOPOLOGY: linear


     (ix) FEATURE:
          (A)  NAME/KEY: CDS
          (B)  LOCATION: 1..30


     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:55:

AGC ACC TAC TAT CCT GAC ACT GTG CAG GGC                                    30
Ser Thr Tyr Tyr Pro Asp Thr Val Gln Gly
 1               5                   10


(2) INFORMATION FOR SEQ ID NO:56:

     (i)  SEQUENCE CHARACTERISTICS:
          (A)  LENGTH: 10 amino acids
          (B)  TYPE: amino acid
          (D)  TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:56:

Ser Thr Tyr Tyr Pro Asp Thr Val Gln Gly
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:57:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..30

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:57:

```
AGC ACC TAC TAT TTA GAC ACT GTG GAG GGC                     30
Ser Thr Tyr Tyr Leu Asp Thr Val Glu Gly
 1               5                   10
```


(2) INFORMATION FOR SEQ ID NO:58:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:58:

```
Ser Thr Tyr Tyr Leu Asp Thr Val Glu Gly
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:59:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..30

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:59:

```
GCA AGA CAT AAC CAT GGC AGT TTT GCT TAC                     30
Ala Arg His Asn His Gly Ser Phe Ala Tyr
 1               5                   10
```


(2) INFORMATION FOR SEQ ID NO:60:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:60:

```
Ala Arg His Asn His Gly Ser Phe Ala Tyr
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:61:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..30

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:61:

```
GCA AGA CAT AAC TAC GGC AGT TAT GCT TAC                    30
Ala Arg His Asn Tyr Gly Ser Tyr Ala Tyr
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:62:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:62:

```
Ala Arg His Asn Tyr Gly Ser Tyr Ala Tyr
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:63:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..30

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:63:

```
GCA AGA CAT AAC TAC GGC AGT TTT GAT TAC                    30
Ala Arg His Asn Tyr Gly Ser Phe Asp Tyr
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:64:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

(ii) MOLECULE TYPE: protein

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:64:

```
Ala Arg His Asn Tyr Gly Ser Phe Asp Tyr
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:65:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..30

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:65:

```
GCA AGA CAT AAC TAC GGC AGT TTT TAT TAC            30
Ala Arg His Asn Tyr Gly Ser Phe Tyr Tyr
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:66:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:66:

```
Ala Arg His Asn Tyr Gly Ser Phe Tyr Tyr
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:67:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..30

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:67:

```
GCA AGA CAT AAC TAC GGC AGT TTT GCT TCT            30
Ala Arg His Asn Tyr Gly Ser Phe Ala Ser
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:68:

    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids

                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear

            (ii) MOLECULE TYPE: protein

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:68:

Ala Arg His Asn Tyr Gly Ser Phe Ala Ser
1   5   10

(2) INFORMATION FOR SEQ ID NO:69:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 30 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: both
            (D) TOPOLOGY: linear

        (ix) FEATURE:
            (A) NAME/KEY: CDS
            (B) LOCATION: 1..30

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:69:

GCA AGA CAT AAC TAC GGC AGT TTT GCT ACT   30
Ala Arg His Asn Tyr Gly Ser Phe Ala Thr
1   5   10

(2) INFORMATION FOR SEQ ID NO:70:

            (i) SEQUENCE CHARACTERISTICS:
                (A) LENGTH: 10 amino acids
                (B) TYPE: amino acid
                (D) TOPOLOGY: linear

            (ii) MOLECULE TYPE: protein

            (xi) SEQUENCE DESCRIPTION: SEQ ID NO:70:

Ala Arg His Asn Tyr Gly Ser Phe Ala Thr
1   5   10

(2) INFORMATION FOR SEQ ID NO:71:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 30 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: both
            (D) TOPOLOGY: linear

        (ix) FEATURE:
            (A) NAME/KEY: CDS
            (B) LOCATION: 1..30

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:71:

GCA AGA CAT AAC TAC GGC AGT TTT GCT GAT   30
Ala Arg His Asn Tyr Gly Ser Phe Ala Asp
1   5   10

(2) INFORMATION FOR SEQ ID NO:72:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:72:

```
Ala Arg His Asn Tyr Gly Ser Phe Ala Asp
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:73:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..30

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:73:

```
GCA AGA CAT AAC TAC GGC AGT TTT GCT GAG        30
Ala Arg His Asn Tyr Gly Ser Phe Ala Glu
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:74:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear

    (ii) MOLECULE TYPE: protein

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:74:

```
Ala Arg His Asn Tyr Gly Ser Phe Ala Glu
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:75:

     (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear

    (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..30

    (xi) SEQUENCE DESCRIPTION: SEQ ID NO:75:

```
GCA AGA CAT AAC TAC GGC AGT TTT GCT ATG        30
Ala Arg His Asn Tyr Gly Ser Phe Ala Met
1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:76:

 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 10 amino acids
  (B) TYPE: amino acid
  (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:76:

```
Ala Arg His Asn Tyr Gly Ser Phe Ala Met
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:77:

 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 30 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: both
  (D) TOPOLOGY: linear

 (ix) FEATURE:
  (A) NAME/KEY: CDS
  (B) LOCATION: 1..30

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:77:

```
GCA AGA CAT AAC TAC GGC AGT TTT GCT GGG                    30
Ala Arg His Asn Tyr Gly Ser Phe Ala Gly
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:78:

 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 10 amino acids
  (B) TYPE: amino acid
  (D) TOPOLOGY: linear

 (ii) MOLECULE TYPE: protein

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:78:

```
Ala Arg His Asn Tyr Gly Ser Phe Ala Gly
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:79:

 (i) SEQUENCE CHARACTERISTICS:
  (A) LENGTH: 30 base pairs
  (B) TYPE: nucleic acid
  (C) STRANDEDNESS: both
  (D) TOPOLOGY: linear

 (ix) FEATURE:
  (A) NAME/KEY: CDS
  (B) LOCATION: 1..30

 (xi) SEQUENCE DESCRIPTION: SEQ ID NO:79:

```
GCA AGA CAT AAC TAC GGC AGT TTT GCT GCT                                    30
Ala Arg His Asn Tyr Gly Ser Phe Ala Ala
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:80:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 10 amino acids
     (B) TYPE: amino acid
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:80:

```
Ala Arg His Asn Tyr Gly Ser Phe Ala Ala
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:81:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 39 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: both
     (D) TOPOLOGY: linear

   (ix) FEATURE:
     (A) NAME/KEY: CDS
     (B) LOCATION: 1..39

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:81:

```
CAG GCC AGC CAA AGT ATT AGC AAC TTT CTA CAC TGG TAT                        39
Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His Trp Tyr
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:82:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 13 amino acids
     (B) TYPE: amino acid
     (D) TOPOLOGY: linear

   (ii) MOLECULE TYPE: protein

   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:82:

```
Gln Ala Ser Gln Ser Ile Ser Asn Phe Leu His Trp Tyr
 1               5                   10
```

(2). INFORMATION FOR SEQ ID NO:83:

   (i) SEQUENCE CHARACTERISTICS:
     (A) LENGTH: 33 base pairs
     (B) TYPE: nucleic acid
     (C) STRANDEDNESS: both
     (D) TOPOLOGY: linear

   (ix) FEATURE:
     (A) NAME/KEY: CDS
     (B) LOCATION: 1..33

(xi) SEQUENCE DESCRIPTION: SEQ ID NO:83:

```
CTT CTC ATC CGT TAT TCT TCC CAG TCC ATC TCT                          33
Leu Leu Ile Arg Tyr Ser Ser Gln Ser Ile Ser
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:84:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 11 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:84:

```
Leu Leu Ile Arg Tyr Ser Ser Gln Ser Ile Ser
 1               5                   10
```

(2) INFORMATION FOR SEQ ID NO:85:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 27 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: both
          (D) TOPOLOGY: linear

     (ix) FEATURE:
          (A) NAME/KEY: CDS
          (B) LOCATION: 1..27

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:85:

```
CAA CAG AGT AAT AGC TGG CCT CAC ACG                                  27
Gln Gln Ser Asn Ser Trp Pro His Thr
 1               5
```

(2) INFORMATION FOR SEQ ID NO:86:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 9 amino acids
          (B) TYPE: amino acid
          (D) TOPOLOGY: linear

     (ii) MOLECULE TYPE: protein

     (xi) SEQUENCE DESCRIPTION: SEQ ID NO:86:

```
Gln Gln Ser Asn Ser Trp Pro His Thr
 1               5
```

(2) INFORMATION FOR SEQ ID NO:87:

      (i) SEQUENCE CHARACTERISTICS:
          (A) LENGTH: 27 base pairs
          (B) TYPE: nucleic acid
          (C) STRANDEDNESS: double
          (D) TOPOLOGY: linear

     (ix) FEATURE:
          (A) NAME/KEY: CDS

            (B) LOCATION: 1..27

       (xi) SEQUENCE DESCRIPTION: SEQ ID NO:87:

CAA CAG AGT ACT AGC TGG CCT CAC ACT   27
Gln Gln Ser Thr Ser Trp Pro His Thr
  1   5

   (2) INFORMATION FOR SEQ ID NO:88:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 9 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:88:

Gln Gln Ser Thr Ser Trp Pro His Thr
  1   5

   (2) INFORMATION FOR SEQ ID NO:89:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 27 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: both
             (D) TOPOLOGY: linear

        (ix) FEATURE:
             (A) NAME/KEY: CDS
             (B) LOCATION: 1..27

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:89:

CAA CAG AGT GGC AGC TGG CCT CTG ACG   27
Gln Gln Ser Gly Ser Trp Pro Leu Thr
  1   5

   (2) INFORMATION FOR SEQ ID NO:90:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 9 amino acids
             (B) TYPE: amino acid
             (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:90:

Gln Gln Ser Gly Ser Trp Pro Leu Thr
  1   5

   (2) INFORMATION FOR SEQ ID NO:91:

        (i) SEQUENCE CHARACTERISTICS:
             (A) LENGTH: 27 base pairs
             (B) TYPE: nucleic acid
             (C) STRANDEDNESS: both
             (D) TOPOLOGY: linear

```
(ix) FEATURE:
     (A) NAME/KEY: CDS
     (B) LOCATION: 1..27
```

```
(xi) SEQUENCE DESCRIPTION: SEQ ID NO:91:
```

```
CAA CAG AGT GGC AGC TGG CCT CAG ACG                          27
Gln Gln Ser Gly Ser Trp Pro Gln Thr
  1           5
```

```
(2) INFORMATION FOR SEQ ID NO:92:
```

```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 9 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
```

```
   (ii) MOLECULE TYPE: protein
```

```
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:92:
```

```
Gln Gln Ser Gly Ser Trp Pro Gln Thr
  1           5
```

```
(2) INFORMATION FOR SEQ ID NO:93:
```

```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
        (D) TOPOLOGY: linear
```

```
   (ix) FEATURE:
        (A) NAME/KEY: CDS
        (B) LOCATION: 1..30
```

```
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:93:
```

```
GCA AGA CAT AAC CAT GGC AGT TTT GCT TCT                       30
Ala Arg His Asn His Gly Ser Phe Ala Ser
  1           5                   10
```

```
(2) INFORMATION FOR SEQ ID NO:94:
```

```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 10 amino acids
        (B) TYPE: amino acid
        (D) TOPOLOGY: linear
```

```
   (ii) MOLECULE TYPE: protein
```

```
   (xi) SEQUENCE DESCRIPTION: SEQ ID NO:94:
```

```
Ala Arg His Asn His Gly Ser Phe Ala Ser
  1           5                   10
```

```
(2) INFORMATION FOR SEQ ID NO:95:
```

```
    (i) SEQUENCE CHARACTERISTICS:
        (A) LENGTH: 30 base pairs
        (B) TYPE: nucleic acid
        (C) STRANDEDNESS: both
```

```
                    (D) TOPOLOGY: linear


          (ix) FEATURE:
                    (A) NAME/KEY: CDS
                    (B) LOCATION: 1..30


          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:95:

GCA AGA CAT AAC CAT GGC AGT TTT TAT TCT                                    30
Ala Arg His Asn His Gly Ser Phe Tyr Ser
 1               5                  10


     (2) INFORMATION FOR SEQ ID NO:96:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 10 amino acids
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: protein

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:96:

Ala Arg His Asn His Gly Ser Phe Tyr Ser
 1               5                  10

     (2) INFORMATION FOR SEQ ID NO:97:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 30 base pairs
                    (B) TYPE: nucleic acid
                    (C) STRANDEDNESS: both
                    (D) TOPOLOGY: linear


          (ix) FEATURE:
                    (A) NAME/KEY: CDS
                    (B) LOCATION: 1..30


          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:97:

GCA AGA CAT AAC TAC GGC AGT TTT TAT GAG                                    30
Ala Arg His Asn Tyr Gly Ser Phe Tyr Glu
 1               5                  10


     (2) INFORMATION FOR SEQ ID NO:98:

          (i) SEQUENCE CHARACTERISTICS:
                    (A) LENGTH: 10 amino acids
                    (B) TYPE: amino acid
                    (D) TOPOLOGY: linear

          (ii) MOLECULE TYPE: protein

          (xi) SEQUENCE DESCRIPTION: SEQ ID NO:98:

Ala Arg His Asn Tyr Gly Ser Phe Tyr Glu
 1               5                  10

     (2) INFORMATION FOR SEQ ID NO:99:
```

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 30 base pairs
            (B) TYPE: nucleic acid
            (C) STRANDEDNESS: both
            (D) TOPOLOGY: linear

        (ix) FEATURE:
            (A) NAME/KEY: CDS
            (B) LOCATION: 1..30

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:99:

GCA AGA CAT AAC TAC GGC AGT TTT TAT TCT   30
Ala Arg His Asn Tyr Gly Ser Phe Tyr Ser
 1   5   10

(2) INFORMATION FOR SEQ ID NO:100:

        (i) SEQUENCE CHARACTERISTICS:
            (A) LENGTH: 10 amino acids
            (B) TYPE: amino acid
            (D) TOPOLOGY: linear

        (ii) MOLECULE TYPE: protein

        (xi) SEQUENCE DESCRIPTION: SEQ ID NO:100:

Ala Arg His Asn Tyr Gly Ser Phe Tyr Ser
 1   5   10